

5' NCT AAA TCA GCC TCT TGC CCC ATT GCT CTT TGC AGG GGT AGA AGA AGG AAG TGT

AGC GGG GTA AGG AAT GCA CCG TCA GGG TCT CTC ACA ACC CTT TCC CAG CTC TCC

TCC CCA ACA AAC AGT ACC TGG GAT GGA GCC CTA GGG TAA TCG CAG CCA CGG GAT

GGG TCG AGG TGA CAG GCT TCA GGG ACC ACA CTT CGG CCT TTG CCC GAC CTT CCA

CAA CTT AAG CGA AGA GAG GCC ACC AGC CGT AAC AGG GCG TTA AAG CCC AGG GGA

AGA TTG GTC CTT ATG ACT TGC TGC CTT CCA GCC CTC AGA TTC ATC GCT ACC CCG

M T C C L P A L R F I A T P

AGG CTA AGC GCC ATG CCT CAT ATT GAC AAC GAT GTG AAA CTG GAC TTC AAG GAT

R L S A M P H I D N D V K L D F K D

GTC CTT TTG AGG CCC AAA CGC AGT ACC CTT AAG TCT CGA AGT GAG GTG GAT CTC

V L L R P K R S T L K S R S E V D L

ACA AGA TCC TTT TCA TTT CGG AAC TCA AAG CAG ACA TAC TCT GGG GTT CCC ATC

T R S F S F R N S K Q T Y S G V P I

ATT GCT GCC AAT ATG GAT ACT GTG GGC ACC TTT GAG ATG GCC AAG GTT CTC TGT

I A A N M D T V G T F E M A K V L C

AAG TTC TCT CTC TTC ACT GCT GTC CAT AAG CAC TAT AGC CTC GTT CAG TGG CAA

K F S L F T A V H K H Y S L V Q W Q

GAG TTT GCT GGC CAG AAT CCT GAC TGT CTT GAG CAT CTG GCT GCC AGC TCA GGC

E F A G Q N P D C L E H L A A S S G

ACA GGC TCT TCT GAC TTT GAG CAG CTG GAA CAG ATC CTG GAA GCT ATT CCC CAG

T G S S D F E Q L E Q I L E A I P Q

FIGURE 1A

711 720 729 738 747 756
 GTG AAG TAT ATA TGC CTG GAT GTG GCA AAT GGC TAC TCT GAA CAC TTT GTT GAA
 V K Y I C L D V A N G Y S E H F V E

765 774 783 792 801 810
 TTT GTA AAA GAT GTA CGG AAG CGC TTC CCC CAG CAC ACC ATC ATG GCA GGG AAT
 F V K D V R K R F P Q H T I M A G N

819 828 837 846 855 864
 GTG GTA ACA GGA GAG ATG GTA GAA GAG CTC ATC CTT TCT GGG GCT GAC ATC ATC
 V V T G E M V E E L I L S G A D I I

873 882 891 900 909 918
 AAA GTG GGA ATT GGG CCA GGC TCT GTG TGT ACT ACT CGG AAG AAA ACT GGA GTG
 K V G I G P G S V C T T R K K T G V

927 936 945 954 963 972
 GGG TAT CCA CAG CTC AGC GCA GTG ATG GAG TGT GCA GAT GCT GCT CAT GGC CTC
 G Y P Q L S A V M E C A D A A H G L

981 990 999 1008 1017 1026
 AAA GGC CAC ATC ATT TCA GAT GGA GGT TGC AGC TGT CCT GGG GAT GTG GCC AAG
 K G H I I S D G G C S C P G D V A K

1035 1044 1053 1062 1071 1080
 GCT TTT GGG GCA GGA GCT GAC TTC GTG ATG CTG GGT GGC ATG CTG GCT GGG CAC
 A F G A G A D F V M L G G M L A G H

1089 1098 1107 1116 1125 1134
 AGT GAG TCA GGT GGT GAG CTC ATC GAG AGG GAT GGC AAG AAG TAC AAG CTC TTC
 S E S G G E L I E R D G K K Y K L F

1143 1152 1161 1170 1179 1188
 TAT GGA ATG AGT TCT GAA ATG GCC ATG AAG AAG TAT GCT GGG GGC GTG GCT GAG
 Y G M S S E M A M K K Y A G G V A E

1197 1206 1215 1224 1233 1242
 TAC AGA GCC TCA GAG GGA AAG ACA GTG GAA GTT CCT TTT AAA GGA GAT GTG GAA
 Y R A S E G K T V E V P F K G D V E

1251 1260 1269 1278 1287 1296
 CAT ACC ATC CGA GAC ATC CTA GGA GGG ATC CGC TCT ACG TGT ACC TAT GTG GGA
 H T I R D I L G G I R S T C T Y V G

1305 1314 1323 1332 1341 1350
 GCA GCT AAG CTC AAA GAG TTG AGC AGG AGA ACT ACC TTC ATC CGA GTC ACC CAG
 A A K L K E L S R R T T F I R V T Q

1359 1368 1377 1386 1395 1404
 CAG GTG AAT CCA ATC TTC AGT GAG GCG TGC TAG ACC TGA GCA GTT CTA CCC TCC
 Q V N P I F S E A C

FIGURE 1B

1413 1422 1431 1440 1449 1458
CAA GGC ACC AGT ACT CTA CCA TGG GGC ATC CCA AGT GGG GTC CTC ACC CAT CCC

1467 1476 1485 1494 1503 1512
AGC TAC TGC AGC TCT GTA TTA CTT TGT CAT TTC CTG TTG TCT CAC TCC TGA GGG

1521 1530 1539 1548 1557 1566
CTC CTG CAG TAA CTC TGT ACT TCT CTA TCT GCA CAC ACA AAA TGC CCA AGG CAC

1575 1584 1593 1602 1611 1620
TCA CTG GGG AGG AAG CAA GGA AGC AAA CAG TCT GAG GAA ATG ATG CAA GAA AAT

1629 1638 1647 1656 1665 1674
CAA ATG GGA ATC TGG GGA CCC AAC ACA ACA TCC TGA AGA TTA TTA AAA GGA AAA

1683 1692 1701 1710 1719 1728
GAT GCT GAT TGG TAC ATA AAT CTT TTA CAT GGC CTT GGT CTA GAG GAG GCA GGC

1737 1746 1755 1764 1773 1782
TTT TAG AAT CAT GTT TTG TTA ATC CGC TTC ACT AAA TTG GAC CTT CAC ATA TCT

1791 1800 1809 1818 1827 1836
AAA AAG CTC TGA AGT GTT TGT ATA TTT GAA ATA CCT CAA TAA AGA GAG AGC TCA

TTG ACT GT 3'

FIGURE 1C

1	M	T	C	C	L	P	A	L	R	F	I	A	T	P	R	L	S	A	M	P	H	I	D	N	D	V	K	L	D	F	K	D	V	L	L	R	P	K	R	S	HQMR
1	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	9473772				
1	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	9544455					
41	T	L	K	S	R	S	E	V	D	L	T	R	S	F	S	F	R	N	S	K	Q	T	Y	S	G	V	P	I	A	A	N	M	D	T	V	G	T	F	E	HQMR	
22	T	L	K	S	R	S	D	V	E	L	E	R	Q	F	T	F	K	H	S	G	Q	S	W	S	G	V	P	I	A	A	N	M	D	T	V	G	T	F	S	9473772	
23	S	L	K	S	R	A	E	V	D	L	E	R	T	F	T	F	R	N	S	K	O	T	Y	S	G	I	P	I	V	A	N	M	D	T	V	G	T	F	E	9544455	
61	M	A	K	V	L	C	K	F	S	L	F	T	A	V	H	K	H	Y	S	L	V	Q	W	Q	E	F	A	G	O	N	P	-	D	C	L	E	H	L	A	HQMR	
62	M	A	S	A	L	A	S	E	D	I	L	T	A	V	H	K	H	Y	S	V	E	E	W	O	A	F	I	N	N	S	S	A	D	V	L	K	H	V	M	9473772	
63	M	A	A	V	M	S	Q	H	S	M	F	T	A	I	H	K	H	Y	S	L	D	D	W	K	L	F	A	T	N	H	P	-	E	C	L	Q	N	V	A	9544455	
120	S	S	G	T	G	S	S	D	F	E	Q	L	E	Q	I	L	E	A	I	P	O	V	K	Y	I	C	L	D	V	A	N	G	Y	S	E	H	F	V	E	HQMR	
102	S	T	G	T	S	D	A	D	F	E	K	T	K	Q	I	L	D	L	N	P	A	L	N	F	V	C	I	D	V	A	N	G	Y	S	E	H	F	V	Q	F	9473772
102	S	S	G	S	G	Q	N	D	L	E	K	M	T	S	I	L	E	A	V	P	O	V	K	F	I	C	L	D	V	A	N	G	Y	S	E	H	F	V	E	9544455	
160	V	K	D	V	R	K	R	F	P	O	H	T	I	M	A	G	N	V	T	G	E	M	V	E	E	L	I	L	S	G	A	D	I	I	K	V	G	I	G	HQMR	
142	V	A	K	A	R	E	A	W	P	T	K	T	I	C	A	G	N	V	T	G	E	M	C	E	E	L	I	L	S	G	A	D	I	V	K	V	G	I	G	9473772	
142	V	K	L	V	R	A	K	F	P	E	H	T	I	M	A	G	N	V	T	G	E	M	V	E	E	L	I	L	S	G	A	D	I	I	K	V	G	V	G	9544455	
200	P	G	S	V	C	T	T	R	K	K	T	G	V	G	Y	P	Q	L	S	A	V	M	E	C	A	D	A	A	H	G	L	K	G	H	I	I	S	D	G	G	HQMR
182	P	G	S	V	C	T	T	R	V	K	T	G	V	G	Y	P	Q	L	S	A	V	I	E	C	A	D	A	A	H	G	L	G	G	M	I	V	I	S	D	G	9473772
182	P	G	S	V	C	T	T	R	T	K	T	G	V	G	Y	P	Q	L	S	A	V	I	E	C	A	D	S	A	H	G	L	K	G	H	I	I	S	D	G	G	9544455
240	C	S	C	P	G	D	V	A	K	A	F	G	A	G	A	D	F	V	M	L	G	G	M	L	A	G	H	S	E	S	G	G	E	L	I	E	R	D	G	K	HQMR
222	C	T	T	P	G	D	V	A	K	A	F	-	A	R	A	D	F	V	M	L	G	G	M	L	A	G	H	E	E	S	G	G	R	I	V	E	E	N	G	E	9473772
222	C	T	C	P	G	D	V	A	K	A	F	G	A	G	A	D	F	V	M	L	G	G	M	F	S	G	H	T	E	C	A	G	E	V	F	E	R	N	G	R	9544455

FIGURE 2A

280	KY	KLFY	GMSSSE	M	A	M	K	K	Y	A	G	G	V	A	E	Y	R	A	S	E	G	K	T	V	E	V	P	F	K	G	D	V	HQMR								
261	KF	M	L	F	Y	G	M	S	S	E	S	A	M	K	R	H	V	G	G	V	A	E	Y	R	A	A	E	G	K	T	V	K	L	P	L	R	G	P	V	g473772	
262	K	L	K	L	F	Y	G	M	S	S	D	T	A	M	N	K	H	A	G	G	V	A	E	Y	R	A	S	E	G	K	T	V	E	V	P	Y	K	G	D	V	g544455
320	E	H	T	I	R	D	I	L	G	G	I	R	S	T	C	T	Y	V	G	A	A	K	L	K	E	L	S	R	R	T	T	F	I	R	V	T	O	Q	V	N	HQMR
301	E	N	T	A	R	D	I	L	G	G	L	R	S	A	C	T	Y	V	G	A	S	R	L	K	E	L	T	K	R	T	T	F	I	R	V	O	E	Q	E	N	g473772
302	E	N	T	I	L	D	I	L	G	G	L	R	S	T	C	T	Y	V	G	A	A	K	L	K	E	L	S	R	R	A	T	F	I	R	V	T	O	Q	H	N	g544455
360	P	I	F	S	E	A	C																															HQMR			
341	R	I	F	N	N	L																																g473772			
342	T	V	F	S																																		g544455			

FIGURE 2B

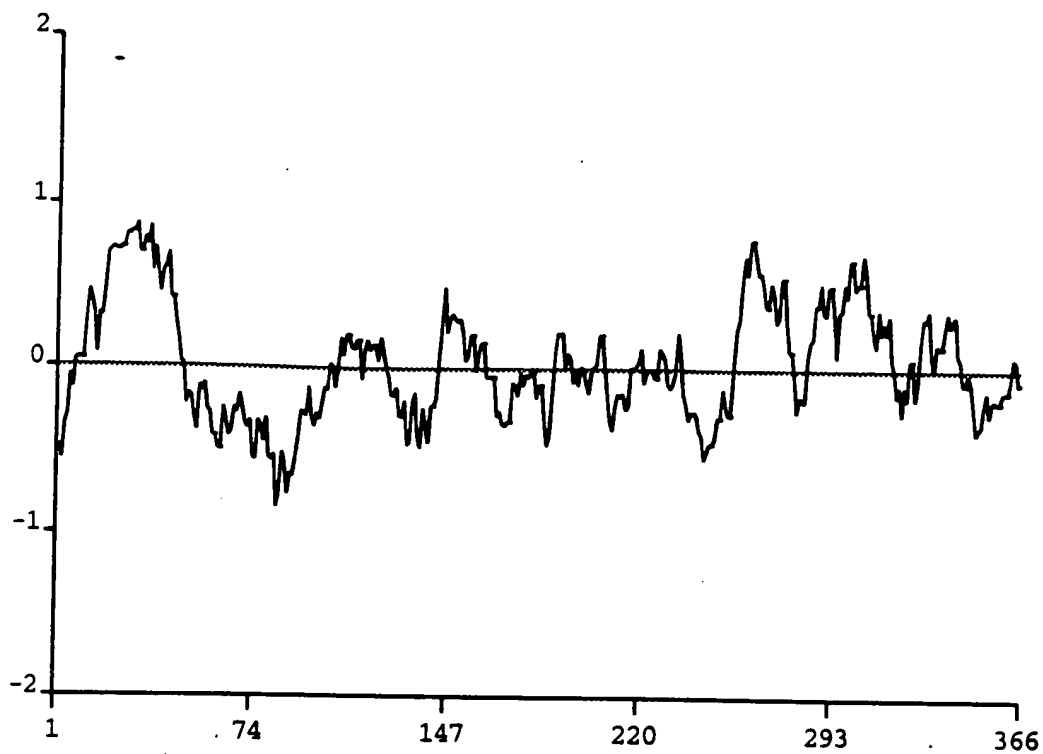


FIGURE 3A

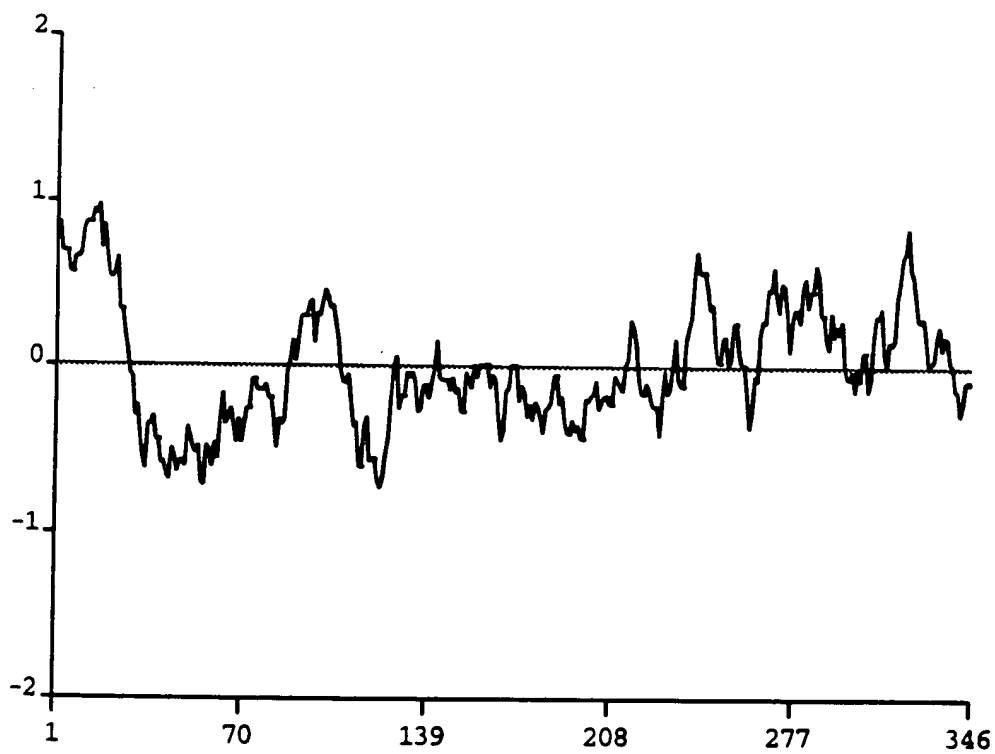


FIGURE 3B

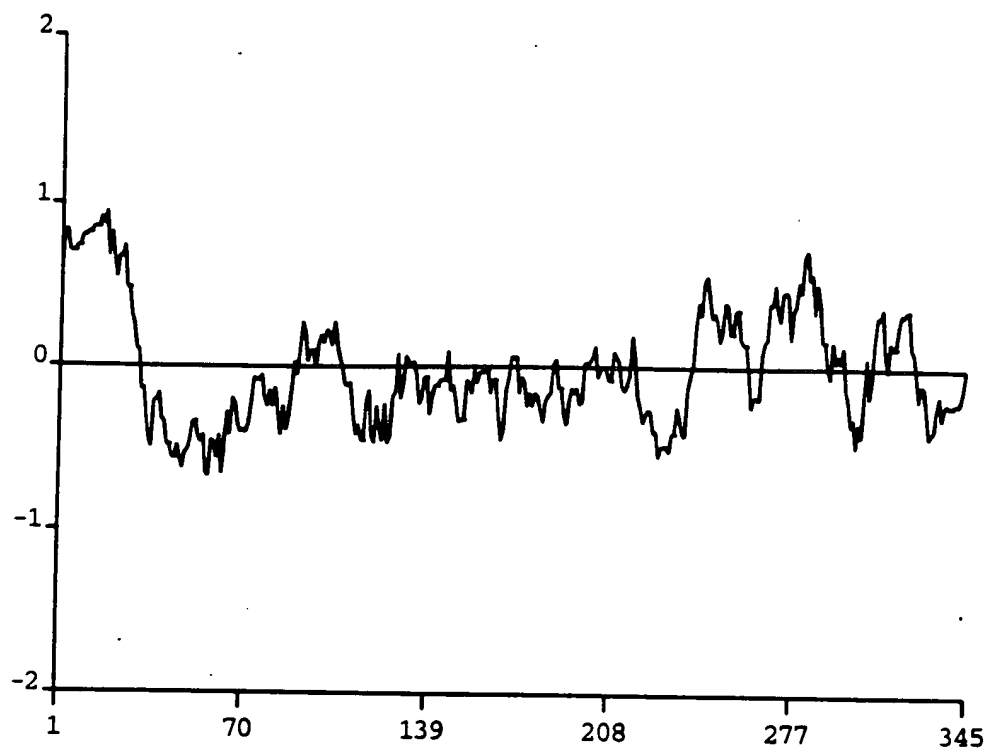


FIGURE 3C

Library	Lib Description	Abun	Pct Abun
MMLR3DT01	macrophages (adher PBMNC), M/F, 72-hr MLR	1	0.0332
ENDCNOT03	endothelial cells, dermal microvascular, neonatal M	1	0.0210
LUNGFEM01	lung, fetal, NORM, WM	1	0.0148
PROSTUT04	prostate tumor, 57 M, match to PROSNOT06	1	0.0117
BRAINOT09	brain, fetal M	1	0.0093
BRAITUT02	brain tumor, metastasis, 58 M	1	0.0075

FIGURE 4